

March 12, 2002

Via DHL

U.S. Patent and Trademark Office Crystal Mall I Seventh Floor, Receptionist Attn: Examiner William Moore, Art Unit 1652 1911 South Clark Street Arlington, VA 22202

Re: U.S. Application No. 09/652,743 filed August 31, 2000

"Proteases and Variants Thereof"

Dear Examiner Moore:

As per your request, enclosed is a computer readable form of the Sequence Listing mailed on October 22, 2001. The content of the paper copy that was filed on October 22, 2001 and of the enclosed computer readable form is the same. This submission contains no new matter.

If you have any questions, please do not hesitate to contact me.

Very truly yours,

Elias J. Lambiris

Director, Patents - US

•	- () 1600 RU
	CRF bors Corrected by the STIC Systems Branch CRF Processing Date: 3/13/20
N	Changed a file from non-ASCII to ASCII ENTERE Tedited by: (STIC's
	Changed the margins in cases where the sequence text was "wrapped" down to the next line.
	Edited a format error in the Current Application Data section, specifically:
	Edited the Current Application Data section with the actual current number. The number inputted by the applicant was the prior application data; or other
	Added the mandatory heading and subheadings for "Current Application Data".
	Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
	Changed the spelling of a mandatory field (the headings or subheadings), specifically:
	Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
	Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
,	Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
	Inserted colons after headings/subheadings. Headings edited included:
	Deleted extra, invalid, headings used by an applicant, specifically:
	Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of file page numbers throughout text; other invalid text, such as
	Inserted mandatory headings, specifically:
	Corrected an obvious error in the response, specifically:
	Edited identifiers where upper case is used but lower case is required, or vice versa.
	Edited ideptifiers where upper case is used but lower case is required, or vice versa. Corrected an error in the Number of Sequences field, specifically:
_	
C	Corrected an error in the Number of Sequences field, specifically:
C	Corrected an error in the Number of Sequences field, specifically: A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted. Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error

^{*}Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95







Input Set : A:\PTO.AMC.txt



```
3 <110> APPLICANT: Norregaard-Madsen, Mads
             Ostergaard, Peter Rahbek
              Christensen, Claus Bo Voge
              Lassen, Soren Flensted
      8 <120> TITLE OF INVENTION: Novel Proteases And Variants Thereof
     10 <130> FILE REFERENCE: 5665.400-US
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/652,743A
C--> 12 <141> CURRENT FILING DATE: 2000-08-31
     12 <160> NUMBER OF SEQ ID NOS: 45
     14 <170> SOFTWARE: PatentIn version 3.1
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     18 <212> TYPE: DNA
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     35 <222> LOCATION: (1)..(93)
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     47 Leu Val Ser Lys Lys Ser Val Lys Arg Gly Leu Ile Thr Gly Leu Ile
                        -90
                                             -85
                                                                                96
     50 ggt att tot att tat tot tta ggt atg cac cog gcc caa gcc gcg cca
     51 Gly Ile Ser Ile Tyr Ser Leu Gly Met His Pro Ala Gln Ala Ala Pro
                    -75
                                         -70
     54 tog cot cat act cot gtt toa ago gat cot toa tao aaa gog gaa aca
     55 Ser Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Ala Glu Thr
                                     -55
                                                                               192
     58 tog gtt act tat gac coa cac att aag ago gat caa tac ggo ttg tat
     59 Ser Val Thr Tyr Asp Pro His Ile Lys Ser Asp Gln Tyr Gly Leu Tyr
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                                                     -35
```





Input Set : A:\PTO.AMC.txt

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66						ccc					tac			aaa Lys -1		gtg	288
70					gat									gca Ala			336
														tgc Cys			384
	Trp													tgc Cys			432
														tcg Ser			480
87 88	Arg	Asn	Gly	Thr 70	Ser	Tyr	Pro	Tyr	Gly 75	Ser	Val	Lys	Ser	acg Thr 80	Arg	Tyr	528
														gat Asp			576
95 96	Āla	Ile 100	Glu	Leu	Ser	Glu	Pro 105	Ile	Gly	Asn	Thr	Val 110	Gly	tac Tyr	Phe	Gly	624
99 100	Tyr 11:	Ser 5	Tyr	Thr	Thr	Ser 120	Ser	Leu	Val	Gly	Thr 12	Thr 5	Val	acc Thr	Ile	Ser 130	672
103 104	Gly	у Ту:	r Pro	o Gly	7 Asp 135	Lys 5	Thi	Ala	a Gly	y Th:	r Gl: O	n Tr	o Gli	n His	s Ser 145		720
107 108	Pro	o Ile	e Ala	a Ile 150	e Sei	Glu	ı Thi	туз	Lys 15	s Lei 5	u Gli	n Ty:	r Ala	a Met 160	Asp	acg Thr	768
111 112	Ty:	r Gl	y Gl	y Gli 5	n Sei	Gly	y Sei	170	va:	l Ph	e Gl	u Gli	n Se:	r Sei 5	s Sei	aga Arg	816
115 116	Thi	r As:	n Cy:	s Sei	r Gly	Pro	Cys 185	s Sei	r Lei	u Al	a Va	l Hi:	s Thi	r Ası	n Gly	y Val	864
119 120	Ту:) 19:	r Gl	y Gl	y Sei	r Sei	туз 200	Ası	n Arg	g Gl	y Th	r Ar	g Ile 5	e Thi	a aaa r Lys	a gaq s Glu	g gtg 1 Val 210	912
123 124	Phe	e As	p As	t tte	Thi 215	c Ası					r Al						948
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Input Set : A:\PTO.AMC.txt

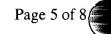
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					Bac	illus	3									
)> SI														
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	Gly	Ile	Ser	Ile -75	Tyr	Ser	Leu	Gly	Met -70	His	Pro	Ala	Gln	Ala -65	Ala	Pro
	Ser	Pro	His	Thr	Pro	Val	Ser	Ser	Asp	Pro	Ser	Tyr	Lys -50	Ala	Glu	Thr
	Ser	Val -45	Thr	Tyr	Asp	Pro	His -40	Ile	Lys	Ser	Asp	Gln -35	Tyr	Gly	Leu	Tyr
150	Ser -30		Ala	Phe	Thr	Gly -25	Thr	Gly	Lys	Val	Asn -20	Glu	Thr	Lys	Glu	Lys -15
		Glu	Lys	Lys	Ser -10		Ala	Lys	Ala	Pro -5		Ser	Ile	Lys -1	Ser 1	
	Ile	Gly	Ser 5	Asp	Asp	Arg	Thr	Arg 10	Val	-	Asn	Thr	Thr 15			Pro
	Tyr	Arg 20	_	Ile	Val	His	Ile 25		Ser	Ser	Ile	Gly 30		Cys	Thr	Gly
	_		Ile	Gly	Pro	Lys 40		Val	Ala	Thr	Ala 45		His	Cys	Ile	Tyr 50
		Thr	Ser	Ser	Gly 55	-	Phe	Ala	Gly	Thr 60		Thr	Val	Ser	Pro 65	-
	Arg	Asn	Gly	Thr 70	Ser	Tyr	Pro	Tyr	Gly 75		Val	Lys	Ser	Thr 80	Arg	Tyr
	Phe	Ile	Pro 85	Ser	Gly	Trp	Arg	Ser 90	Gly	Asn	Thr	Asn	Tyr 95	Asp	Tyr	Gly
182 183	Ala	Ile 100	Glu	Leu	Ser	Glu	Pro 105	Ile	Gly	Asn	Thr	Val 110	Gly	Tyr	Phe	Gly
186	Tyr 115	Ser	Tyr	Thr	Thr	Ser 120	Ser	Leu	Val	Gly	Thr 125	Thr	Val	Thr	Ile	Ser 130
		Tyr	Pro	Gly	Asp 135	Lys	Thr	Ala	Gly	Thr 140	Gln	Trp	Gln	His	Ser 145	Gly
	Pro	Ile	Ala	Ile 150	Ser	Glu	Thr	Tyr	Lys 155	Leu	Gln	Tyr	Ala	Met 160	Asp	Thr
	Tyr	Gly	Gly 165	Gln	Ser	Gly	Ser	Pro 170	Val	Phe	Glu	Gln	Ser 175	Ser	Ser	Arg
	Thr	Asn 180	Cys	Ser	Gly	Pro	Cys 185	Ser	Leu	Ala		His 190		Asn	Gly	Val
	Tyr 195		Gly	Ser	Ser	Tyr 200	Asn	Arg	Gly	Thr	Arg 205		Thr	Lys	Glu	Val 210
		Asp	Asn	Leu	Thr 215		Trp	Lys	Asn	Ser 220	Ala	Gln				
	<21	0> SI	EQ II	ON C	: 3											
215	<21	1> L	ENGT	H: 10	026											
		2> T														
					Bac	illu	S									
219	<22	0> F	EATU	RE:												





Input Set : A:\PTO.AMC.txt

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	222	<223	ro <	THER	INFO	RMAT	ION											
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		<2213				mat	pept	ide										
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		<220																
		<221				sia	nent	-ide										
		<222																
		<223																
		<220				ו אויייונ	LION	•										
r.r \						220	nont	-140										
W>		<221		-		_												
		<2222																
		<223					TON											
		<400																4.5
		atg								ct tt								45
		Met	Lys	Leu	ı Leı	ı Let	-		eu Ti	nr Ph	ne Va			.ıe ı	he N	let l	Leu	
		-120					-11					_	110					
																	tt act	93
			Gly	/ Ile	e Lei	ı Sei			al As	sn Al	La Ti			a G	lu Th	ır Le	eu Thr	
		-105					-1(_	95				-90	
		aaa 1																141
	253	Lys 1	Leu	Asn	Lys	Ile	Ser	Gln	Lys	Gln	Glu	Pro	Ser	Tyr	Lys	Leu	Asp	
	254					-85					-80					-75		
	256	gaa (gaa	atg	gat	tat	gtt	cta	att	gat	ttg	gaa	aca	caa	tct	gaa	tcg	189
	257	Glu (Glu	Met	Asp	Tyr	Val	Leu	Ile	Asp	Leu	Glu	Thr	Gln	Ser	Glu	Ser	
	258				-70					-65					-60			
	260	att a	att	tcg	ata	gga	gat	aat	acc	gat	ttg	gga	gat	caa	tcg	ttt	act	237
	261	Ile :	Ile	Ser	Ile	Gly	Asp	Asn	Thr	Asp	Leu	Gly	Asp	Gln	Ser	Phe	Thr	
	262			- 55		_			-50					-45				
	264	tct 1	tta	qqq	aaq	gtg	gga	cat	gga	qaa	ctt	gag	aaa	att	aac	tta	gaa	285
		Ser 1																
	266		-40	•	-		-	-35	•				-30					
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		Glu 1																
	270			,			-20					-15					-10	
		cct	att	αaa	caa	aaa		aσc	cct.	ttt	at.t.	at.t.	ata	aac	gat.	gat	aaa	381
		Pro :																
	274	110 .		O L u	0.2.11	-5	110	001	110	-1		,		U -1	5	110[0-1	
		aga a	ana	саа	att	-	aat	act	tct			cca	+++	cat	-	ctt	act	429
		Arg A																123
	278	nig /	лту	10	Val	GIII	LOII	1111	15	rnc	ncc	110	1110	20	1114	пси	1111	
		tat a	a + +		+++	~~~	220	a++		a ort	202	taa	a ort		tot	aas	aat	477
																		4//
		Tyr :		GIU	rne	стХ	ASII		THE	ser.	T 11 T.	ıτħ	35	СУБ	per.	ату	дтй	
	282		25	~		~-+	++-	30	~++	~ ~ +	a = +	~~~		+~+	a+ -	~~~	aa+	525
		gtg a																525
		Val	тте	GTÀ	Tnr	Asp		vaı	val	Tnr	asn		HIS	Cys	val	GIU		
	286	40					45					50					55	







RAW SEQUENCE LISTING PATENT APPLICATION: US/09/652,743A DATE: 03/13/2002 TIME: 16:47:06

Input Set : A:\PTO.AMC.txt

				_			-	gtt			_			-			573
	Ser	Val	Leu	Ala	_	Thr	Val	Val	Pro	_	Met	Asn	Asn	Ser		Trp	
290					60					65					70		(21
	_						-	act	_					-			621
293	Ala	туг	СТА	H1S	тут	Arg	vaı	Thr	80 GTU	тте	TTE	туг	Pro	ASP 85	GIII	туг	
	ana	aat	aac		act	tca	ααα	ttt		tat	act	ata	ctt		αta	aca	669
								Phe									000
298	1119	11511	90		1110	JCI	Olu	95	p	- 1 -		110	100	9	141	1114	
	cct	qac		gat	qqa	cat	cat	att	qqa	aac	aga	qct		att	tta	tct	717
								Ile									
302		105		-	-	_	110		•			115	-				
304	ttt	aca	gaa	aca	gga	act	gtt	aac	gaa	aat	act	ttt	cta	aga	acg	tat	765
305	Phe	Thr	Glu	Thr	Gly	Thr	Val	Asn	Glu	Asn	Thr	Phe	Leu	Arg	Thr	Tyr	
306	120					125					130					135	
308	gga	tac	CCC	ggt	gat	aaa	ata	tca	gag	aca	aaa	tta	att	tct	ttg	tgg	813
309	Gly	Tyr	Pro	Gly	Asp	Lys	Ile	Ser	Glu	Thr	Lys	Leu	Ile	Ser	Leu	Trp	
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		_	_		-		-	gca		_		_	-		_		861
	Gly	Met	Val	_	Arg	Ser	Asp	Ala		Leu	His	Arg	Asp		Leu	Phe	
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	Tyr	Asn		Asp	Thr	Tyr	Phe	Gly	Gln	Ser	GLY	Ser		Val	Leu	Asn	
318			170					175					180				057
	_	_	-		_	_		gtt			-						957
	ser		Asp	ser	мет	vaı		Val	HIS	ASI	Ата	195	туг	тте	vaı	GIY	
322	aat	185	200	~ ~ ~	2++	22+	190	ggt	aat	222	ato		202	a a t	+++	2.72	1005
								Gly									1003
	200	N 3 II	Arg	Glu	110	205	GIY	GIY	110	цуз	210	nrg	nrg	пор	TITC	215	
		tta	+++	aat	caa		aac				210					213	1026
		Leu				_											
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341	-120					-11						110					
	Ser	_	y Ile	e Lei	ı Se			al As	sn Al	la Tl			la Gi	lu T	nr Le	eu Thr	
	-109				_	-10			_	_		95			_	-90	
	Lys	Leu	Asn	Lys		Ser	Gln	Lys	Gln		Pro	Ser	Tyr	Lys		Asp	
349		~ 1		_	-85		_	_,	_	-80	~ 1	m 1	- 1	_	-75		
	GLu	GLu	мet	_	туr	val	ьeu	Ile		ьeu	GLu	Thr	GIn		GLU	ser	
353	т1	т1	0	-70	C1	7 ~~	7 ~ ~	mh~	-65	T 0	C1	7 ~~	C1~	-60	Dha	mhr.	
	тте	тте	-55	тте	сту	ASP	ASN	Thr	ASP	ьeu	стХ	ASP	-45	ser	Pne	THE	
357	C0~	T CV		Tura	Wa I	C1**	uic	Gly	C1	LON	C1	T ***		λας	Lou	Glu	
200	Set	neu	оту	пЛэ	val	GTA	ura	оту	GIU	ьец	GIU	пys	TIE	USII	цеu	GIU	

DATE: 03/13/2002 RAW SEQUENCE LISTING ERROR SUMMARY PATENT APPLICATION: US/09/652,743A

TIME: 16:47:07

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\03132002\1652743A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:18; N Pos. 21,36

Seq#:20; N Pos. 12,15,18,21,24

Seg#:21; Xaa Pos. 2

Seq#:22; N Pos. 22,25,31

Seq#:23; Xaa Pos. 5

Seq#:24; N Pos. 15,18

Seq#:25; Xaa Pos. 6

Seq#:38; N Pos. 18,21,27

Seq#:39; Xaa Pos. 2,4

Seq#:40; N Pos. 12,15,21

Seq#:44; N Pos. 14,15









1600

RAW SEQUENCE LISTING DATE: 03/13/2002 PATENT APPLICATION: US/09/652,743A TIME: 16:16:04 Input Set : A:\sequence.ST25.txt Output Set: N:\CRF3\03132002\1652743A.raw 3 <110> APPLICANT: Norregaard-Madsen, Mads Ostergaard, Peter Rahbek Christensen, Claus Bo Voge Lassen, Soren Flensted 8 <120> TITLE OF INVENTION: Novel Ptoteases And Variants Thereof 10 <130> FILE REFERENCE: 5665.400-US C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/652,743A C--> 12 <141> CURRENT FILING DATE: 2000-08-31 12 <160> NUMBER OF SEQ ID NOS: 45 14 <170> SOFTWARE: PatentIn version 3.1 Doss Not Comply 16 <210> SEQ ID NO: 1 17 <211> LENGTH: 948 Corrected Diskette Needed 18 <212> TYPE: DNA 19 <213> ORGANISM: Bacillus 21 <220> FEATURE: 22 <221> NAME/KEY: CDS 23 <222> LOCATION: (1)..(948) 24 <223> OTHER INFORMATION: 27 <220> FEATURE: 28 <221> NAME/KEY: mat_peptide 29 <222> LOCATION: (283)..() 30 <223> OTHER INFORMATION: 33 <220> FEATURE: 34 <221> NAME/KEY: sig_peptide 35 <222> LOCATION: (1)..(93) 36 <223> OTHER INFORMATION: 39 <220> FEATURE: W--> 40 <221> NAME/KEY: pro-peptide 41 <222> LOCATION: (94)..(282) 42 <223> OTHER INFORMATION: 45 <400> SEQUENCE: 1 46 ttg gtt agt aaa aag agt gtt aaa cga ggt ttg atc aca ggt ctc att 48 47 Leu Val Ser Lys Ser Val Lys Arg Gly Leu Ile Thr Gly Leu Ile 48 -90 -85 -80 50 ggt att tot att tat tot tta ggt atg cac ccg gcc caa gcc gcg cca 96 51 Gly Ile Ser Ile Tyr Ser Leu Gly Met His Pro Ala Gln Ala Ala Pro -75 -70 54 tcg cct cat act cct gtt tca agc gat cct tca tac aaa gcg gaa aca 144 55 Ser Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Ala Glu Thr -60 - 55 -50 58 tcg gtt act tat gac cca cac att aag agc gat caa tac ggc ttg tat 192

59 Ser Val Thr Tyr Asp Pro His Ile Lys Ser Asp Gln Tyr Gly Leu Tyr

-45

60



Input Set : A:\sequence.ST25.txt

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	- 30					-25					-20					-15	
					tca												288
	Ala	Glu	Lys	Lys	Ser	Pro	Ala	Lys	Ala		Tyr	Ser	Ile	Lys	Ser	Val	
68					-10					- 5				- 1	1		
					gat				-					-		_	336
71	Ile	Gly	Ser	Asp	Asp	Arg	Thr	Arg	Val	Thr	Asn	Thr	Thr	Ala	Tyr	Pro	
72			5					10					15				
		_			gtt				_	_				_			384
75	Tyr	Arg	Ala	Ile	Val	His	Ile	Ser	Ser	Ser	Ile	Gly	Ser	Cys	Thr	Gly	
76		20					25					30					
78	tgg	atg	atc	ggt	ccg	aaa	acc	gtc	gca	aca	gcc	gga	cac	tgc	atc	tat	432
79	Trp	Met	Ile	Gly	Pro	Lys	Thr	Val	Ala	Thr	Ala	Gly	His	Cys	Ile	Tyr	
80	35					40					45					50	
					ggt												480
83	Asp	Thr	Ser	Ser	Gly	Ser	Phe	Ala	Gly	Thr	Ala	Thr	Val	Ser	Pro	Gly	
84					55					60					65		
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87	Arg	Asn	Gly	Thr	Ser	Tyr	Pro	Tyr	Gly	Ser	Val	Lys	Ser	Thr	Arg	Tyr	
88				70				,	75					80			
90	ttt	att	ccg	tca	gga	tgg	aga	agc	gga	aac	acc	aat	tac	gat	tac	gga	576
91	Phe	Ile	Pro	Ser	Gly	Trp	Arg	Ser	Gly	Asn	Thr	Asn	Tyr	Asp	Tyr	Gly	
92			85					90					95				
94	gca	atc	gaa	cta	agc	gaa	ccg	atc	ggc	aat	act	gtc	gga	tac	ttc	gga	624
95	Ala	Ile	Glu	Leu	Ser	Glu	Pro	Ile	Gly	Asn	Thr	Val	Gly	Tyr	Phe	Gly	
96		100					105					110					
98	tac	tcg	tac	act	act	tca	tca	ctt	gtt	ggg	aca	act	gtt	acc	atc	agc	672
	_		Tyr	Thr	Thr	Ser	Ser	Leu	Val	Gly	Thr	Thr	Val	Thr	Ile	Ser	
100) 115	i				120)				125					130	
102	ggc	: tac	c cca	ggc	: gat	aaa	a ca	ı gca	a ggc	aca	a caa	tgg	g cag	g cat	tca	gga	720
	_	Туг	Pro) Gly	/ Asp	Lys	Thr	Ala	a Gly	Thr	: Gln	Trp	Glr	n His	s Ser	Gly	
104					135					140					145		
																acg	768
107	Pro) Il∈	e Ala	ı Ile	Ser	Glu	Thr	Tyr			ı Gln	Туг	Ala	Met	Asp	Thr	
108				150					155					160			
																aga	816
	_	Gly	_		ser Ser	Gly	' Ser			Phe	e Glu	Glr	ı Sei	Ser	Ser	Arg	
112			165					170					175				
																gta	864
				Ser	Gly	Pro			Leu	Ala	ı Val			Asn	Gly	Val	
11ϵ		180					185					190					
																gtg	912
			gly,	Ser	Ser			Arg	, Gly	Thr			Thr	: Lys	Glu	Val	
	195					200					205					210	
					acc												948
		Asp	Asn	Leu	Thr		Trp	Lys	Asn			Gln	ì				
124					215					220)						
127	<21	0> S	EQ I	D NC): 2												



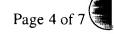


RAW SEQUENCE LISTING PATENT APPLICATION: US/09/652,743A DATE: 03/13/2002 TIME: 16:16:04

Input Set : A:\sequence.ST25.txt

Output Set: N:\CRF3\03132002\1652743A.raw

128 <211> LENGTH: 316 129 <212> TYPE: PRT 130 <213> ORGANISM: Bacillus 132 <400> SEQUENCE: 2 134 Leu Val Ser Lys Lys Ser Val Lys Arg Gly Leu Ile Thr Gly Leu Ile -90 -85 -80 138 Gly Ile Ser Ile Tyr Ser Leu Gly Met His Pro Ala Gln Ala Ala Pro -70 142 Ser Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Ala Glu Thr 143 -60 -55 -50 146 Ser Val Thr Tyr Asp Pro His Ile Lys Ser Asp Gln Tyr Gly Leu Tyr 147 - 45 - 40 - 35 150 Ser Lys Ala Phe Thr Gly Thr Gly Lys Val Asn Glu Thr Lys Glu Lys -25 -20 154 Ala Glu Lys Lys Ser Pro Ala Lys Ala Pro Tyr Ser Ile Lys Ser Val 155 -10 -5 -1 1 158 Ile Gly Ser Asp Asp Arg Thr Arg Val Thr Asn Thr Thr Ala Tyr Pro 10 162 Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly 25 166 Trp Met Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Ile Tyr 4.0 45 170 Asp Thr Ser Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly 171 55 60 174 Arg Asn Gly Thr Ser Tyr Pro Tyr Gly Ser Val Lys Ser Thr Arg Tyr 75 178 Phe Ile Pro Ser Gly Trp Arg Ser Gly Asn Thr Asn Tyr Asp Tyr Gly 90 182 Ala Ile Glu Leu Ser Glu Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly 183 100 105 186 Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Thr Thr Val Thr Ile Ser 120 125 190 Gly Tyr Pro Gly Asp Lys Thr Ala Gly Thr Gln Trp Gln His Ser Gly 135 140 194 Pro Ile Ala Ile Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Met Asp Thr 155 198 Tyr Gly Gln Ser Gly Ser Pro Val Phe Glu Gln Ser Ser Ser Arg 199 165 170 202 Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val 185 190 203 180 206 Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys Glu Val 207 195 200 205 210 Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala Gln 214 <210> SEQ ID NO: 3 215 <211> LENGTH: 1026 216 <212> TYPE: DNA 217 <213> ORGANISM: Bacillus 219 <220> FEATURE:







Input Set : A:\sequence.ST25.txt

	220	<22	1> N	AME/	KEY:	CDS												
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	222	<22	3> 0'	THER	INF	ORMA'	TION	:										
·	225	<220	0> F	EATU:	RE:													
	226	<22	1> N.	AME/	KEY:	mat.	_pep	tide										
	227	<222	2> L	OCAT	ION:	(36	1)	()										
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	231	<220	0> F	EATU:	RE:													
	232	<22	1> N	AME/	KEY:	sig	_pep	tide										
				OCAT														
	234	<223	3> 0'	THER	INF	ORMA'	TION	:										
	237	<220	0> F	EATU!	RE:													
W>	238	<22	1> N	AME/	KEY:	pro	-pep	tide										
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	243	< 400)> S	EQUE!	NCE:	3												
	244	atg	aaa	a cta	a cta	a tta	a aa	a c	tt a	ct t	tt g	ta to	gc a	ata	ttt.	atg	tta	45
	245	Met	Ly:	s Lei	u Lei	u Lei	ı Ly:				-	al C	-					
	246	-120)				-1	15				-]	110					
	248	agt	gg	g at	t cta	a tco	c cca	a g	ta aa	ac g	ca a	ct ca	aa go	ct ga	ag a	ct c	tt act	93
	249	Ser	Gl	y Ile	e Lei	ı Se:	r Pro										eu Thr	
	250	-105					-10						95				-90	
	252	aaa	tta	aat	aaa	ata	agt	cag	aag	cag	gaa	cca	tca	tat	aaa	cta	gat	141
												Pro						
	254					-85					-80			_	_	-75	_	
	256	gaa	gaa	atg	gat	tat	gtt	cta	att	gat	ttg	gaa	aca	caa	tct	gaa	tcg	189
												Glu						
	258				-70					-65					-60			
	260	att	att	tcg	ata	gga	gat	aat	acc	gat	ttg	gga	gat	caa	tcg	ttt	act	237
	261	Ile	Ile	Ser	Ile	Gly	Asp	Asn	Thr	Asp	Leu	Gly	Asp	Gln	Ser	Phe	Thr	
	262			- 55					~50					-45				
												gag						285
	265	Ser	Leu	Gly	Lys	Val	Gly	His	Gly	Glu	Leu	Glu	Lys	Ile	Asn	Leu	Glu	
	266		-40					- 35					- 30					
												gac						333
			Phe	Arg	Asn	Pro		Leu	Thr	Val	Val	Asp	Pro	Leu	Thr	Arg	Lys	
	270						-20					-15					-10	
												gtt						381
	273	Pro				_						Val		_	-	_	Gly	
	274					_				_	_				-			
												cca						429
		Arg	Arg		Val	Gln	Asn	Thr		Phe.	Met	Pro	Phe	Arg	Ala	Leu	Thr	
	278			10					15					20				
												tgg						477
		Tyr		Glu	Phe	Gly	Asn		Thr	Ser	Thr	Trp		Cys	Ser	Gly	Gly	
	282		25					30					35					
												gca						525
			Ile	Gly	Thr	Asp		Val	Val	Thr	Asn	Ala	His	Cys	Val	Glu	_	
	286	40					45					50					55	

Input Set : A:\sequence.ST25.txt

Output Set: N:\CRF3\03132002\1652743A.raw

					-						-						
288	tct	gtg	tta	gca	ggt	act	gta	gtt	cct	ggt	atg	aac	aat	agt	cag	tgg	573
	Ser			-			-	-			_			_	_		
290					60					65					70		
	gca																621
	Ala	Tyr	Gly		Tyr	Arg	Val	Thr		Ile	Ile	Tyr	Pro	-	Gln	Tyr	
294				75					80					85			
	aga																669
	Arg	ASN	90	GTÀ	АТА	ser	GIU	95	Asp	Tyr	Ата	ile		Arg	vaı	Ala	
298	cct	a 2 a		a a t	aas	og+	aa t		aaa	220	2022	aat	100	- + +	++>	tat	717
	Pro	-		_		_					_	_					/ 1 /
302		105	261	изь	GLY	AIG	110	116	СТУ	ASII	ALY	115	СТУ	116	цеu	261	
	ttt		gaa	aca	ααa	act.		aac	gaa	aat	act.		cta	aga	acq	t.a.t.	765
	Phe																
	120				_	125					130			,		135	
308	gga	tac	ccc	ggt	gat	aaa	ata	tca	gag	aca	aaa	tta	att	tct	ttg	tgg	813
	Gly																
310					140					145					150		
	gga																861
	Gly	Met	Val	_	Arg	Ser	Asp	Ala		Leu	His	Arg	Asp		Leu	Phe	
314				155					160					165			
	tac													-			909
	Tyr	Asn		Asp	Thr	Tyr	Phe	-	GIn	Ser	GIŸ	Ser		Val	Leu	Asn	
318	200	~+-	170	+	n + ~	~++	~~~	175	an+	t	~~~		180	a + a	~++		0.5.7
	agc Ser										_				-		957
322		185	АЗР	261	мес	vai	190	val	птъ	ASII	ніа	195	тут	116	vai	СТУ	
	ggt		agg	gaa	att	aat		aat	cct	aaa	atc		aga	gat	+++	aca	1005
	Gly											_	_	_			1005
	200		,			205	4	1		1	210	5	- 5			215	
328	aac	tta	ttt	aat	caa	atg	aac										1026
329	Asn	Leu	Phe	Asn	Gln	Met	Asn										
330					220												
	<210																
	<21				12												
	<217				D	: 11	_										
	<213 <400					LIIUS	3										
	Met					1 T.376	. T.	יוב יוב	ar Dh	10 V:	.1 C	, c	ום ד	he N	Act I	. 011	
	-120		з псс	и псс	LUC	-11		-u 11	11 11	10 10		10	LIC I	iic i	100 1	Jeu	
			/ Ile	e Leu	ı Sei			al As	sn Al	la Th			la Gl	Lu Th	ır Le	eu Thr	
	-109					-10					- 9					-90	
348	Lys	Leu	Asn	Lys	Ile	Ser	Gln	Lys	Gln	Glu	Pro	Ser	Tyr	Lys	Leu	Asp	
349					-85					- 80					-75		
	Glu	Glu	Met	Asp	Tyr	Val	Leu	Ile		Leu	Glu	Thr	Gln	Ser	Glu	Ser	
353				-70					-65					-60			
	Ile	Ile		Ile	Gly	Asp	Asn		Asp	Leu	Gly	Asp		Ser	Phe	Thr	
357		-	- 55	_				-50	.		a 2		-45	_	_	~ 1	
360	Ser	Leu	Gly	Lуs	val	GTÀ	Hls	GTA	GLu	Leu	G1u	Lys	тте	Asn	Leu	Glu	



The of a and/or Yna has been detected in the Sequence listing the first the Sequence Listing to mount a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY PATENT APPLICATION: US/09/652,743A DATE: 03/13/2002 TIME: 16:16:05

Input Set : A:\sequence.ST25.txt

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 \dot{\textbf{L}}:40 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:238 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:452~M:257~W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:650 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:840 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEO ID#:9
L:1038 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:1222 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
L:1459 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1515 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:1534 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1565 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1584 M:341 W: (46) "n" or "Xaa" used, for SEO ID#:23
L:1609 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1628 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1847 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:1872 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:1903 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:1965 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
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